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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/011,307

DATE: 06/04/2002 MAR 05 2004  
TIME: 14:54:03

Input Set : A:\0008.app

Output Set: N:\CRF3\06042002\I011307.raw

TECH CENTER 1600/2900

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Zabeau, Marc

7 Vos, Pieter

8 Simons, Guus

10 (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI

12 (iii) NUMBER OF SEQUENCES: 12

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: SPENCER & FRANK

16 (B) STREET: 1100 New York Avenue, N.W., Suite 300 East

17 (C) CITY: Washington

18 (D) STATE: DC

19 (E) COUNTRY: USA

20 (F) ZIP: 20005

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/011,307

C--> 30 (B) FILING DATE: 01-Jul-1988

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: EP 95401849.5

35 (B) FILING DATE: 07-AUG-1995

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Gollin, Michael A.

39 (B) REGISTRATION NUMBER: 31,957

40 (C) REFERENCE/DOCKET NUMBER: GUPLA 0008

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 202-414-4000

44 (B) TELEFAX: 202-414-4040

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 19 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: other nucleic acid

56 (A) DESCRIPTION: /desc = "primer"

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63 GACTGCGTAC CAATTCNNN

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65 (2) INFORMATION FOR SEQ ID NO: 2:  
67 (i) SEQUENCE CHARACTERISTICS:  
68 (A) LENGTH: 19 base pairs  
69 (B) TYPE: nucleic acid  
70 (C) STRANDEDNESS: single  
71 (D) TOPOLOGY: linear  
73 (ii) MOLECULE TYPE: other nucleic acid  
74 (A) DESCRIPTION: /desc = "primer"  
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
81 GATGAGTCCT GAGTAANN  
83 (2) INFORMATION FOR SEQ ID NO: 3:  
85 (i) SEQUENCE CHARACTERISTICS:  
86 (A) LENGTH: 17 base pairs  
87 (B) TYPE: nucleic acid  
88 (C) STRANDEDNESS: single  
89 (D) TOPOLOGY: linear  
91 (ii) MOLECULE TYPE: other nucleic acid  
92 (A) DESCRIPTION: /desc = "oligonucleotide"  
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
99 CTCGTAGACT GCGTACC  
101 (2) INFORMATION FOR SEQ ID NO: 4:  
103 (i) SEQUENCE CHARACTERISTICS:  
104 (A) LENGTH: 18 base pairs  
105 (B) TYPE: nucleic acid  
106 (C) STRANDEDNESS: single  
107 (D) TOPOLOGY: linear  
109 (ii) MOLECULE TYPE: other nucleic acid  
110 (A) DESCRIPTION: /desc = "oligonucleotide"  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
117 AATTGGTACG CAGTCTAC  
119 (2) INFORMATION FOR SEQ ID NO: 5:  
121 (i) SEQUENCE CHARACTERISTICS:  
122 (A) LENGTH: 16 base pairs  
123 (B) TYPE: nucleic acid  
124 (C) STRANDEDNESS: single  
125 (D) TOPOLOGY: linear  
127 (ii) MOLECULE TYPE: other nucleic acid  
128 (A) DESCRIPTION: /desc = "oligonucleotide"  
133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
135 GACGATGAGT CCTGAG  
137 (2) INFORMATION FOR SEQ ID NO: 6:  
139 (i) SEQUENCE CHARACTERISTICS:  
140 (A) LENGTH: 14 base pairs  
141 (B) TYPE: nucleic acid  
142 (C) STRANDEDNESS: single  
143 (D) TOPOLOGY: linear  
145 (ii) MOLECULE TYPE: other nucleic acid  
146 (A) DESCRIPTION: /desc = "oligonucleotide"  
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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153 TACTCAGGAC TCAT
155 (2) INFORMATION FOR SEQ ID NO: 7:
157     (i) SEQUENCE CHARACTERISTICS:
158         (A) LENGTH: 16 base pairs
159         (B) TYPE: nucleic acid
160         (C) STRANDEDNESS: single
161         (D) TOPOLOGY: linear
163     (ii) MOLECULE TYPE: other nucleic acid
164         (A) DESCRIPTION: /desc = "primer"
169     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
171 GACTGCGTAC CAATTC
173 (2) INFORMATION FOR SEQ ID NO: 8:
175     (i) SEQUENCE CHARACTERISTICS:
176         (A) LENGTH: 16 base pairs
177         (B) TYPE: nucleic acid
178         (C) STRANDEDNESS: single
179         (D) TOPOLOGY: linear
181     (ii) MOLECULE TYPE: other nucleic acid
182         (A) DESCRIPTION: /desc = "primer"
187     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
189 GATGAGTCCT GAGTAA
191 (2) INFORMATION FOR SEQ ID NO: 9:
193     (i) SEQUENCE CHARACTERISTICS:
194         (A) LENGTH: 19 base pairs
195         (B) TYPE: nucleic acid
196         (C) STRANDEDNESS: single
197         (D) TOPOLOGY: linear
199     (ii) MOLECULE TYPE: other nucleic acid
200         (A) DESCRIPTION: /desc = "primer"
205     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
207 GACTGCGTAC CAATTCAGA
209 (2) INFORMATION FOR SEQ ID NO: 10:
211     (i) SEQUENCE CHARACTERISTICS:
212         (A) LENGTH: 19 base pairs
213         (B) TYPE: nucleic acid
214         (C) STRANDEDNESS: single
215         (D) TOPOLOGY: linear
217     (ii) MOLECULE TYPE: other nucleic acid
218         (A) DESCRIPTION: /desc = "primer"
223     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
225 GATGAGTCCT GAGTAATCT
227 (2) INFORMATION FOR SEQ ID NO: 11:
229     (i) SEQUENCE CHARACTERISTICS:
230         (A) LENGTH: 6658 base pairs
231         (B) TYPE: nucleic acid
232         (C) STRANDEDNESS: single
233         (D) TOPOLOGY: linear
235     (ii) MOLECULE TYPE: cDNA
238     (ix) FEATURE:

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239      (A) NAME/KEY: CDS
240      (B) LOCATION: 1798..5595
243      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
245 AAAAAAGCAG CTTTAAAAAA AGTACTTTKG AAAGGKGCTG AAAC TTATTT TTTGAAATAA      60
247 GCAGTTATGT GTTTGGAAWA AAAGTGCTGA AGTTGCTATG TCAAACATGA AAAGGGRAAA      120
249 AATGGAAGAA AGAGWTGTTA GGGTTATGTC GTAATTTGGA GATTGTATAA AAATATTAAG      180
251 GGCAAAAAAA ATAAAAATGT GTCAACTTAA AACAGCTTAT AAGCTAAAAAG TTAAAAGCTG      240
253 GGGTAGAGGT GTTTTTTTTT TTTT TAGCTT ATAAGTTGTT TTAAGTTGAC CACATTTTTTA      300
255 TTTT TKTG CTTAATATT TTTATACAAT CTCAAAAATTA CGACATAACC CTAACATCTT      360
257 TTTCTCCCAT TTTTCTCTT TCACGTTTGA CATAGCAACT TCAGCACTTT TATCCAAACA      420
259 CATAACTGCT TATTTTAAAA ATAAGTTTCA GCACTTTCAA AAGTACTTTT TTAAAGCTGC      480
261 TTTTATTAAG CCCATCCAAA CGGGCCCTAA AATTGCTAAT GTTTGCTCTT TCTATTCTCA      540
263 AACTCCGTAA TATTTAAGAA AATTGCTAA TGATAGGTCA CTTTAAACAC TAAATAATTA      600
265 TAAATTGGGT AGAAATTTAT TTATCATTTT AAGCTTTTTT AATTTTGAGT CTTCTCCCTA      660
267 ATTAAGACCC TTCCCCTCTT GCTTCAATTA TTTAACTGAA TAGTCTTTGT CTTATTGTTG      720
269 GGTGAAAGTC TGTCTTCTTG TTAGGTACTA AGTCCTACAA TAATATCAAT AATTTGCTAT      780
271 GGAGAAAAAA ATATTATAGG AGAAAAATAA TTAATTTTAA TTCATGAATA TGTCTTAATA      840
273 TGCAACTCAT TTTGCTTATA TATATCAAAT TAAACTCTGT TCCTTTAACT TTTTCTTATG      900
275 AAGATACATT TTAATTTATT TGATGAGGTT AGTTTTGAAA TTTATATTAT AATAATGAAA      960
277 TGATATAACT TAAAAGAAGT TGTTTGATAT CTTATCAGAA TCATGCAGGT ACTCATAATA      1020
279 TAAGAAATAA TTATGATGAA ATTTATATAT GTTTTATGCA GAGATTTATT ACGCATTGTT      1080
281 TACTTGGGTT ATGTATTACT TATTTTCTCT TTTATCAGAA TGTAATAATA TCATTCAATA      1140
283 AGAAATCCAA TTCTGTAAAA TTCAAAATAC AAACAATAAC ATTTTCAAGA CCGATTTTTT      1200
285 GCCCAAGAAT ATACAGTAAA CATATTTATG ATATGGTAGG TCTCTTTAGT AATTGACCAA      1260
287 CAAGGATTGT GGTGGAGTGG GAAATACTCT TTAATACTTC ACCAAGAGGT CTCCAATTTG      1320
289 AGCCCCTGAA TACGAAATCG TCTTTGTTAG TATATACCTT AACCTAATAC AAAAATTAGT      1380
291 ATATTAGCCT TNACAGCTAA AATCTTTGTG ACCTGTAAGT CACGCGAGGA CAAATTTACC      1440
293 GTAACACCAA CTTATTCATG ATATAATTGT CCCTTTTAGC ACGGTAATAA TGAGGTGGGT      1500
295 AGAAATTTAT TACTTGAGGG CCCTTTCTAC ACCCACCTT ATTCTCTTGC TTCAATTATT      1560
297 GAATTGAAGA AGTAATGAAA AAACAGACTC CATTGGATAA AGGACAGTTT GCAAACACAG      1620
299 CTGTAACAAT TTAGAGCACT AGCAAAATAG AGAGAGTTT GAGAGAAATT TTTGTTTGCA      1680
301 AATTACTCTT AACCTTCAGC AGGTAAAATA AAGTTCTTAA CTGAGACTAT TTGAAGATAT      1740
303 ATTTTGTTAA AGAATCATTT TGTGTGTTTC CTTGTTTGC TTTTGCAGAT TTGAGAA      1797
305 ATG GAG ATT GGC TTA GCA GTT GGT GGT GCA TTT CTC TCC TCA GCT TTG      1845
306 Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu
307 1 5 10 15
309 AAT GTT CTG TTT GAT AGG CTT GCT CCT AAC GGT GAT CTG CTC AAC ATG      1893
310 Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met
311 20 25 30
313 TTT CGG AAG CAT AAG GAT CAT GTT AAG CTC TTA AAG AAG CTG AAA ATG      1941
314 Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Lys Leu Lys Met
315 35 40 45
317 ACT TTG CGT GGT ATT CAG ATT GTG CTA AGT GAT GCA GAG AAT AAG CAA      1989
318 Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln
319 50 55 60
321 GCA TCA AAT CCA TCT GTG AGA GAC TGG CTT AAT GAG CTT CGA GAT GCT      2037
322 Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala
323 65 70 75 80
325 GTC GAC TCT GCT GAA AAT TTA ATA GAA GAA GTC AAT TAT GAA GCT TTG      2085

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326	Val	Asp	Ser	Ala	Glu	Asn	Leu	Ile	Glu	Glu	Val	Asn	Tyr	Glu	Ala	Leu	
327					85				90					95			
329	AGG	CTT	AAG	GTG	GAA	GGT	CAG	CAT	CAG	AAT	TTT	TCA	GAA	ACA	AGC	AAC	2133
330	Arg	Leu	Lys	Val	Glu	Gly	Gln	His	Gln	Asn	Phe	Ser	Glu	Thr	Ser	Asn	
331				100					105					110			
333	CAG	CAA	GTA	AGT	GAT	GAT	TTT	TTC	CTT	AAC	ATA	AAG	GAC	AAG	CTG	GAA	2181
334	Gln	Gln	Val	Ser	Asp	Asp	Phe	Phe	Leu	Asn	Ile	Lys	Asp	Lys	Leu	Glu	
335				115				120					125				
337	GAC	ACT	ATT	GAA	ACA	TTA	AAG	GAT	TTG	CAA	GAG	CAA	ATT	GGT	CTC	CTT	2229
338	Asp	Thr	Ile	Glu	Thr	Leu	Lys	Asp	Leu	Gln	Glu	Gln	Ile	Gly	Leu	Leu	
339				130				135					140				
341	GGC	TTA	AAG	GAG	TAT	TTT	GAT	TCC	ACG	AAA	CTA	GAA	ACT	AGA	AGA	CCT	2277
342	Gly	Leu	Lys	Glu	Tyr	Phe	Asp	Ser	Thr	Lys	Leu	Glu	Thr	Arg	Arg	Pro	
343	145					150					155					160	
345	TCA	ACT	TCT	GTG	GAT	GAT	GAA	TCT	GAT	ATC	TTT	GGT	AGG	CAG	AGC	GAA	2325
346	Ser	Thr	Ser	Val	Asp	Asp	Glu	Ser	Asp	Ile	Phe	Gly	Arg	Gln	Ser	Glu	
347				165					170					175			
349	ATA	GAG	GAT	TTG	ATT	GAC	CGT	CTA	TTG	TCT	GAA	GGT	GCA	AGT	GGG	AAA	2373
350	Ile	Glu	Asp	Leu	Ile	Asp	Arg	Leu	Leu	Ser	Glu	Gly	Ala	Ser	Gly	Lys	
351				180					185					190			
353	AAG	CTG	ACA	GTA	GTT	CCT	ATC	GTT	GGA	ATG	GGC	GGC	CAG	GGC	AAG	ACA	2421
354	Lys	Leu	Thr	Val	Val	Pro	Ile	Val	Gly	Met	Gly	Gly	Gln	Gly	Lys	Thr	
355				195				200					205				
357	ACA	CTT	GCT	AAA	GCC	GTA	TAC	AAT	GAT	GAG	AGG	GTG	AAG	AAT	CAT	TTT	2469
358	Thr	Leu	Ala	Lys	Ala	Val	Tyr	Asn	Asp	Glu	Arg	Val	Lys	Asn	His	Phe	
359				210				215				220					
361	GAT	TTG	AAA	GCG	TGG	TAT	TGC	GTT	TCT	GAA	GGA	TTT	GAT	GCT	TTG	AGA	2517
362	Asp	Leu	Lys	Ala	Trp	Tyr	Cys	Val	Ser	Glu	Gly	Phe	Asp	Ala	Leu	Arg	
363	225					230				235					240		
365	ATA	ACA	AAA	GAA	TTA	CTC	CAA	GAA	ATT	GGC	AAA	TTT	GAC	TCG	AAG	GAT	2565
366	Ile	Thr	Lys	Glu	Leu	Leu	Gln	Glu	Ile	Gly	Lys	Phe	Asp	Ser	Lys	Asp	
367				245					250					255			
369	GTC	CAC	AAC	AAT	CTT	AAC	CAG	CTT	CAA	GTC	AAA	TTG	AAG	GAA	AGT	TTG	2613
370	Val	His	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Val	Lys	Leu	Lys	Glu	Ser	Leu	
371				260					265					270			
373	AAG	GGA	AAG	AAG	TTC	CTT	ATT	GTT	TTG	GAT	GAT	GTG	TGG	AAT	GAA	AAT	2661
374	Lys	Gly	Lys	Lys	Phe	Leu	Ile	Val	Leu	Asp	Asp	Val	Trp	Asn	Glu	Asn	
375				275				280					285				
377	TAC	AAC	GAG	TGG	AAT	GAC	TTG	AGA	AAT	ATT	TTT	GCA	CAA	GGA	GAT	ATA	2709
378	Tyr	Asn	Glu	Trp	Asn	Asp	Leu	Arg	Asn	Ile	Phe	Ala	Gln	Gly	Asp	Ile	
379				290			295					300					
381	GGA	AGT	AAG	ATC	ATT	GTG	ACG	ACA	CGC	AAA	GAC	AGT	GTT	GCC	TTG	ATG	2757
382	Gly	Ser	Lys	Ile	Ile	Val	Thr	Thr	Arg	Lys	Asp	Ser	Val	Ala	Leu	Met	
383	305					310					315				320		
385	ATG	GGA	AAT	GAG	CAA	ATT	CGC	ATG	GGC	AAT	TTG	TCT	ACC	GAA	GCC	TCT	2805
386	Met	Gly	Asn	Glu	Gln	Ile	Arg	Met	Gly	Asn	Leu	Ser	Thr	Glu	Ala	Ser	
387				325					330					335			
389	TGG	TCT	TTA	TTT	CAA	AGA	CAT	GCA	TTT	GAA	AAC	ATG	GAT	CCT	ATG	GGA	2853
390	Trp	Ser	Leu	Phe	Gln	Arg	His	Ala	Phe	Glu	Asn	Met	Asp	Pro	Met	Gly	

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]